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GWGPTPRAGRAALQLKLRRLTELLGAQDGALLVRLLQALRVARMPLERSVRERFLPVH

Fig. 1

100
90
80
70
60
50
40
30
20
10
0

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Fig. 2

CCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGGCCACTACACG
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GCCGCTGCCGCACCGGCTTCGCGCACGCTGGTTCTGCTGGAGCAC
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GCACTGGCTTCCCCCTCAGCACCAAGGTACCAAGGAGCTGAGGAGTGTGAG
CGTGCCGTATCGACTTGTGGCTTCCAGGACATCTCCAT

Fig. 3

SEQ ID No:4	128	CCGGAGACAGCCCCACGACGTGTGGCCCCGTGTCCACCGCCCACTACACG
SEQ ID No:5	1	CCGGAGACAGCCCCACGACGTGTGGCCCCGTGTCCACCGCCNACTACACG
SEQ ID No:6	1	G
SEQ ID No:3	1	GCCGAGACAGCCCCACGACGTGTGGCCCCGTGTCCACCGCCCACTACACG

SEQ ID No: 5	101	GGAGCNTGAGGAGGGCANGNGCTTGCACGCCACAAACCGCCCT
SEQ ID No: 6	52	GGAGCCGTGAGGAGGGCACGGGCTTGCACGCCACAAACCGCCCT
SEQ ID No: 7	1	GAGGGGGCCCCAGGGAGTGGTGGGGAGGGTGGGGAGGGTGG
SEQ ID No: 3	101	GGAGCCGTGAGGAGGGCACGGGCTTGCACGCCACAAACCGCCCT

SEQ ID NO: 5	201	GCATCGTCCACCTGCTGNGGGTGATTGCNCCGGCACCCCCAGCCA
SEQ ID NO: 6	152	GCATCGTCCACCTGCTGGCGGTGATTNCCCCGGCACCCCCAGCCA
SEQ ID NO: 7	82	CAGTCCCCCTGACCCCTGTTCCCTGGCTGGCAGGCCACCCCCAGCCA
SEQ ID NO: 8	1	GCATCGTCCACCTGGCTGGGGCACCCCCAGCCA
SEQ ID NO: 10	1	CTTGTCCACCTGGTGGGGGTGATTNCCC - GGGCACCCCCAGCCA
SEQ ID NO: 3	201	GCATCGTCCACCTGCTGGGGGTGATTGCCCCAGCCA

Fig. 4.

SEQ ID No:5	251	GAACACGCA - TGCAAAGCCGTG
SEQ ID No:7	132	GAACACGGCAGN - CC - AGCCGTGCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No:8	51	GAACACGGCAG - GCCTAGGCCGTGCCAGGCCACCTTCTCAGCCAGCAGC
SEQ ID No:10	47	GAACACGGCAGTGCC - AGCCNT - CCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No:9	1	AGCNGTGCNCNNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID No:3	251	GAACACGGCAGTGCCTAGGCCGTGCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No:7	182	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGCCT
SEQ ID No:8	101	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGCCT
SEQ ID No:10	97	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGNC-T
SEQ ID No:9	36	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGCCT
SEQ ID No:3	301	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGCCT
SEQ ID No:7	232	GGCCCTCAATGTGCCAGGGCTTCCTCCCATGACACCCCTGTGCACCCAG
SEQ ID No:8	151	GGCCCTCAATGTGCCAGGGCTTCCTCCCATGACACCCCTGTGCACCCAGCT
SEQ ID No:10	147	GGCCCTCAATGTGCCAGGGCTTCCTCCCATGACACCCCTGTGCACCCAGCT
SEQ ID No:9	86	GGCCCTCAATGTGCCAGGGCTTCCTCCCATGACACCCCTGTGCACCCAGCT
SEQ ID No:3	351	GGCCCTCAATGTGCCAGGGCTTCCTCCCATGACACCCCTGTGCACCCAGCT
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SEQ ID No:9	136	GCACTGGCTTCCCCCTCAGCACCCAGGTANCGGAGCTGAGGAGTGTGAG
SEQ ID No:3	401	GCACTGGCTTCCCCCTCAGCACCCAGGTACCGAGGCTGAGGAGTGTGAG
SEQ ID No:10	247	CGTGCCTCATCGACTTTGGCTTCCAGGACATCTCCAT
SEQ ID No:9	186	CGTGCCTCATCGACTTTGGCTTCCAGGACATCTCCAT
SEQ ID No:3	451	CGTGCCTCATCGACTTTGGCTTCCAGGACATCTCCAT

Fig. 4. (Cont.)

DNA 30942 M R A L C G P G I S L L C E V I A L P A L I L P V P A V R G V A I I P I Y P W F O A E I G
 hINFR2 I M A P V A V W A A L A V G L E L W A A A M A L P A Q V A F T P Y A P L N G S I C R L R E Y Y D O I

DNA 30942 CRD1 CRD2
 hINFR2 I S E R L V C A D C P P C T F V Q R P C R R O S P T I T C G P C P P R H Y E O F W H Y L E R C R Y C N V L
 I A Q M C C S K C S P G Q H A K V F C T X T S D T V C D S C E O S T Y T O I W N W V P E C L S C G S R

DNA 30942 CRD2 CRD3
 hINFR2 I 95 C G E R E E E A R A C H A T H R A C R C R T G F F - - - A H A G - - F C L E H A S C P P G A G V
 100 C S S D O V E T O A C T R E O N R I C T C R P G W Y C A L S K Q E G C R L C A P L R K C R P G F G V

DNA 30942 CRD3 CRD4
 hINFR2 I 139 I A P G T P S Q N T Q C Q P C P P G T F S A S S S S E Q C O P H R H N C T A L G L A L H V P G S S S
 150 A R P G T E T S D V V C K P C A P G T F S N T T S S T D I C R P H Q I C H V V A - - - I P G N A S

DNA 30942 CRD4
 hINFR2 I 189 H O T L C T S C T G F P L S T R V P G A E E C E R A V I D F V A F Q D I S I K R L O R L L Q A L E A
 196 R O A V C T S T S - - P T A S H A P G A V H L P O P V S T R S Q H T Q P T P E P S T A P S T S F L L

DNA 30942 239 P E G W G P T P - - R A G R A A L O L K L R R R L T E L L G A Q Q G A L L V R L L Q A L R V A R M P
 hINFR2 244 P M G P S P P A E G S T G O F A L P V G L I V G V T A L G L L I I G V V H C V I M T Q V K K K P L -

DNA 30942 287 G L E R S V R E R E L P V H
 hINFR2 293 C L O R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A P S S S S S L E S S A S A L O R R A

hINFR2 343 P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T Q V N V T C I V N V C S S S O

hINFR2 393 H S S Q C S S Q A S S T H G D T D S S P S E S P K D E Q V P F S K E E C A F R S Q L E T P E T L G

hINFR2 443 S T E E K P L P L G V P D A G M K P S

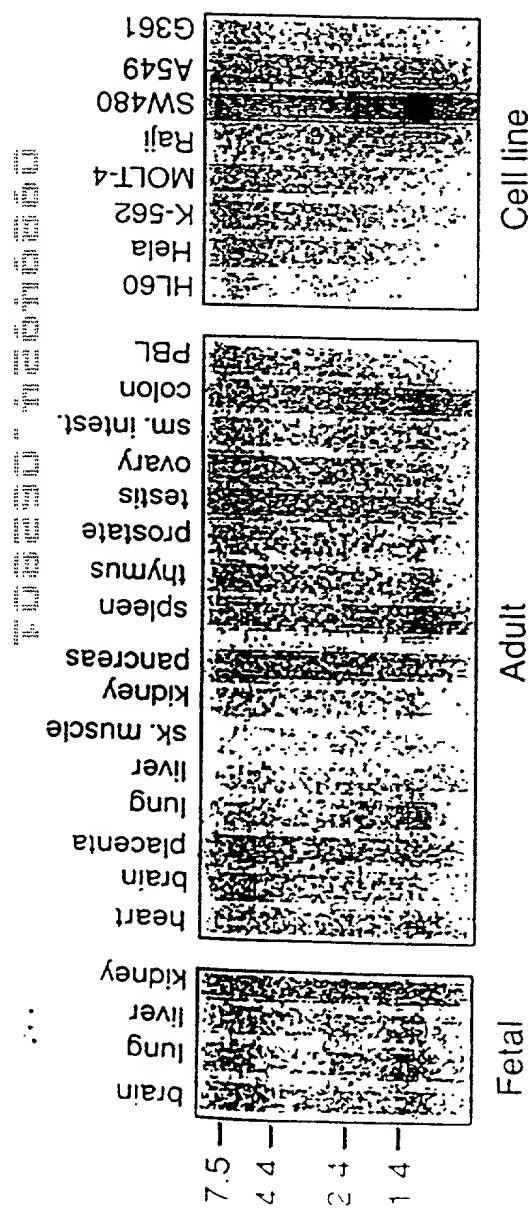
Fig. 5

(

DcR3	1	M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A	31
OPG	1	M N K L L C C A L V F L D I S I K W T T Q E T F P - - - - -	25
<hr/>			
DcR3	32	E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C	62
OPG	26	- ; P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C	54
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DcR3	63	R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V	93
OPG	55	T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P	85
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DcR3	94	L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G	124
OPG	86	V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E	116
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DcR3	125	F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P	155
OPG	117	F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D	147
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DcR3	156	G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S	186
OPG	148	G F F S N E T T S S K A P C R K H T N C S V F G L L L T Q K G N	178
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DcR3	187	S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D	217
OPG	179	A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R	208
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DcR3	218	F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R	247
OPG	209	F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R	239
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DcR3	248	A G R A A L Q L K L R R R L T E L L L G A Q D G A L - L V R L L	277
OPG	240	I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I	270
<hr/>			
DcR3	278	Q A L R V A R M P G L E R S V R E R F L P V H 300	
OPG	271	I Q D I D L C E N S V Q R H I G H A N L T F E 293...	

Fig. 6

Fig. 1



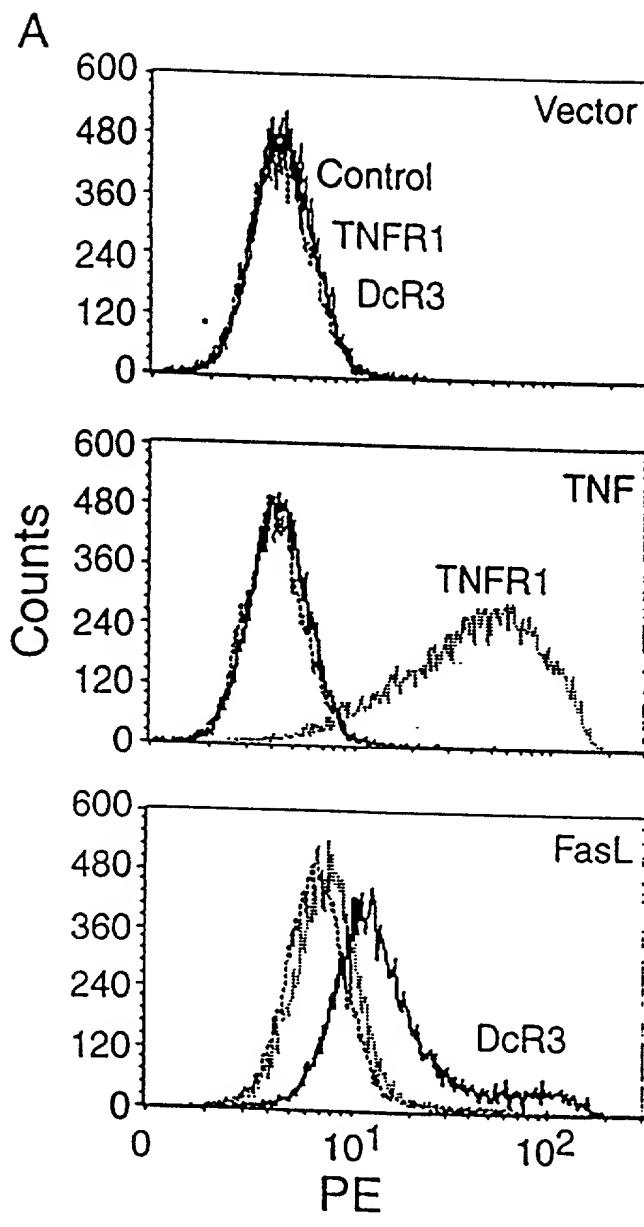
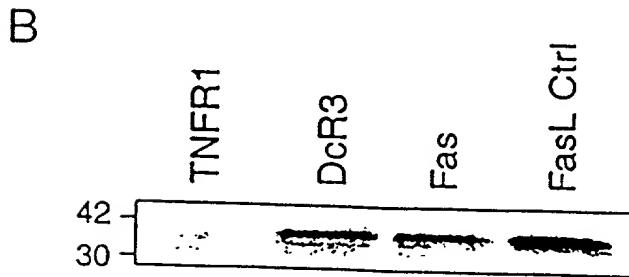


Fig. 8



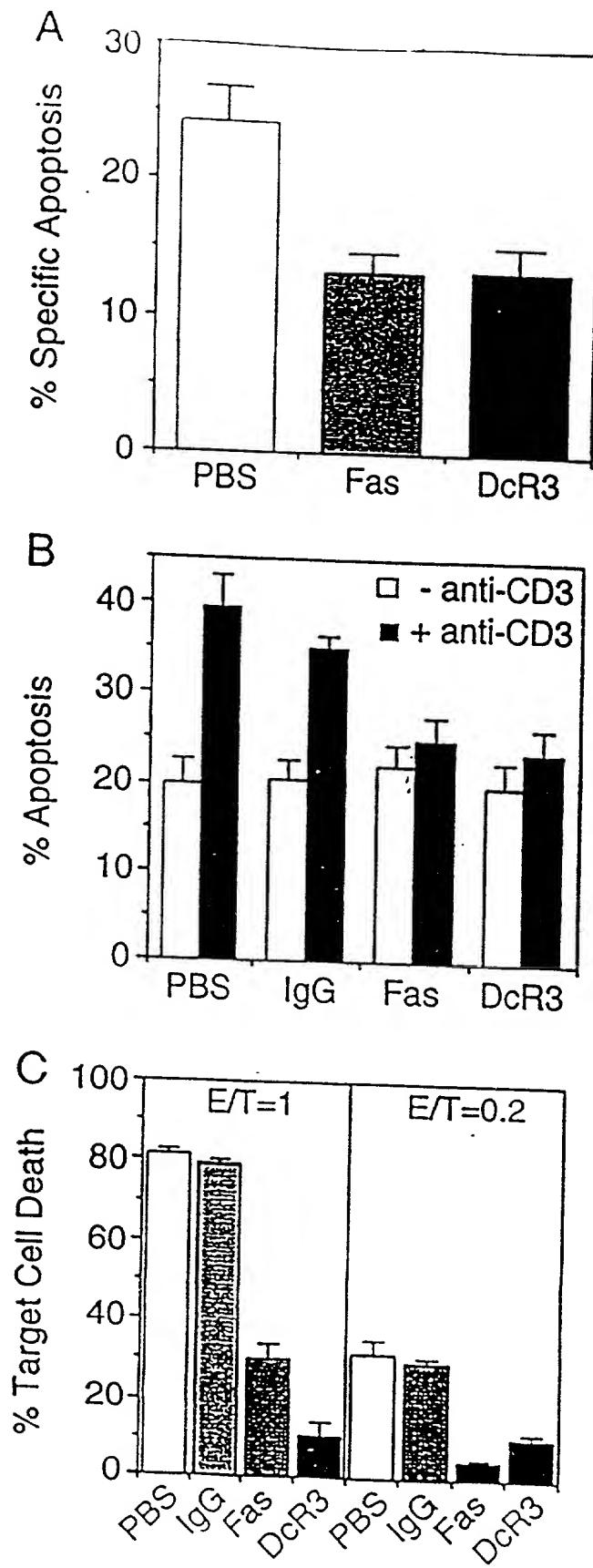


Fig. 9

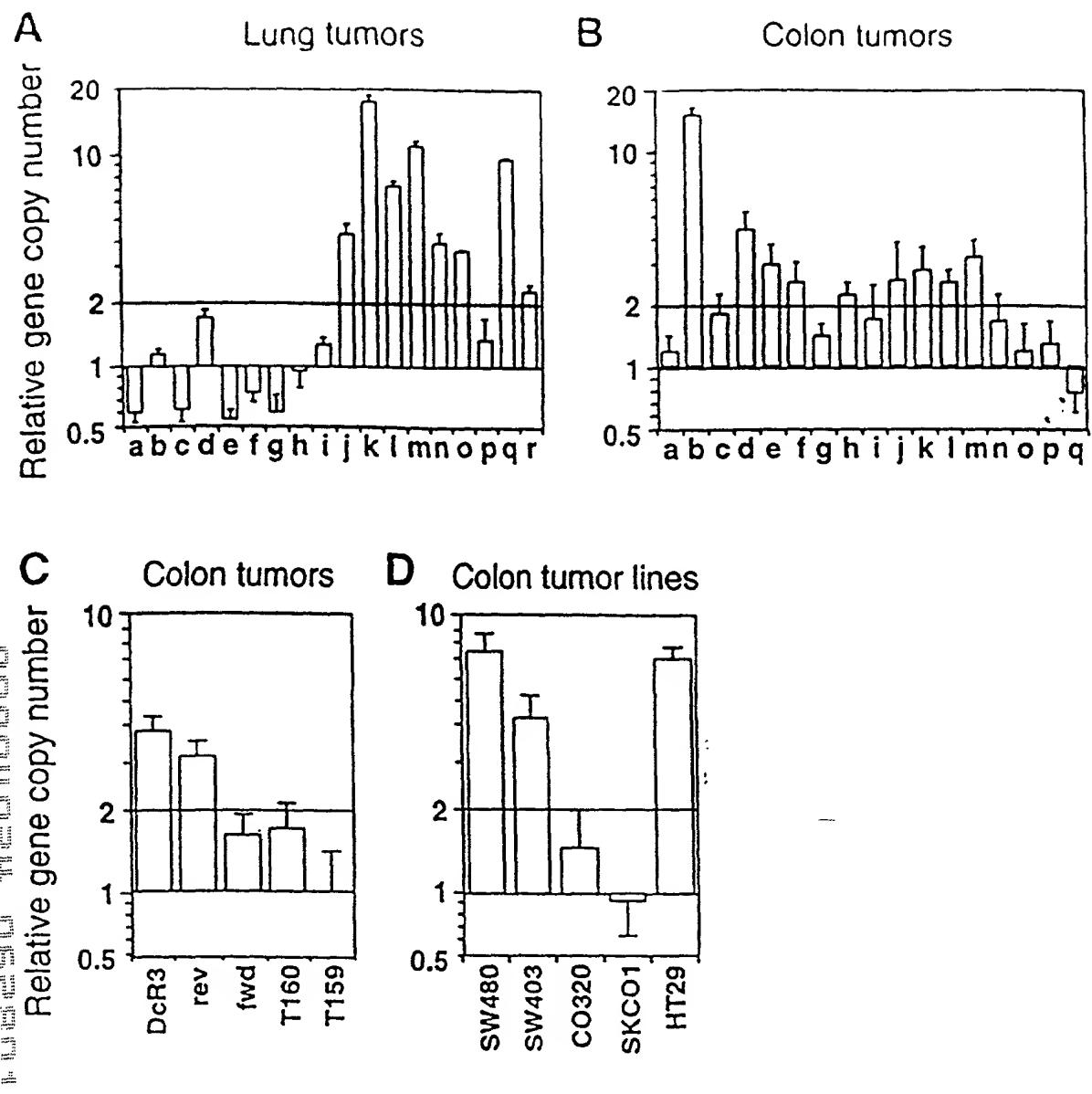


Fig. 10

Fig. 11A

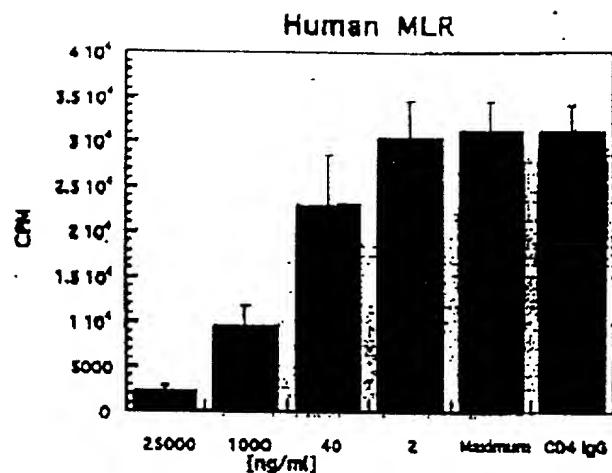


Fig. 11B

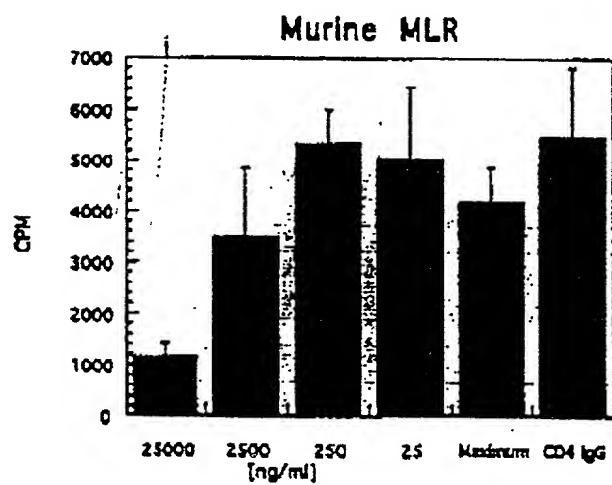


Fig. 11C

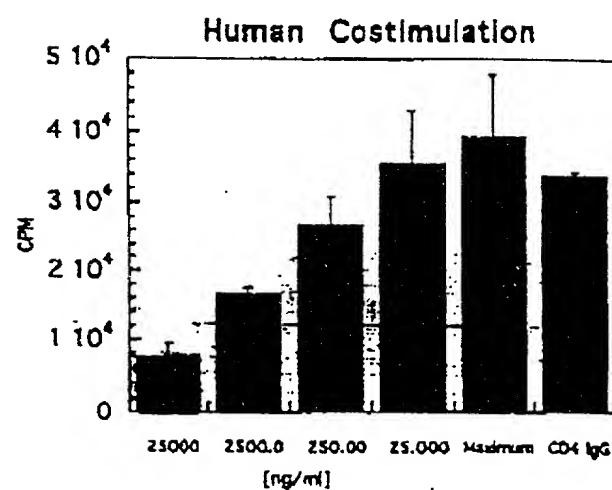


FIGURE 12

<u>mAb</u>	<u>Isotype</u>	Antigen Specificity (ELISA)					阻断活性 (ELISA)
		DcR3	DR4	DR5	DcR1	OPG	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

* blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

Fig. 13

Legend:
—□— 4B7, I, 1
—●— 4C4, I, 4
—■— 5C4, I, 7
—△— 8D3, I, 5
—○— 11C5, I, 2, 8

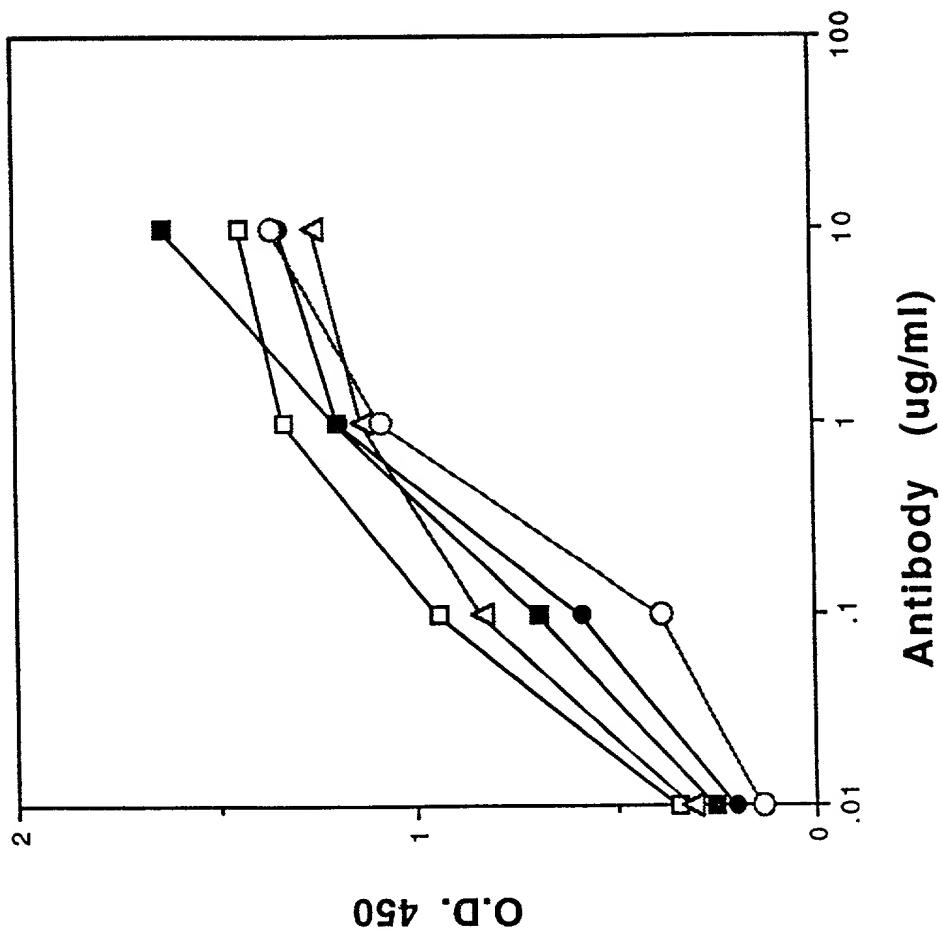


Fig. 14

